

Please amend the application as follows:

In the Specification

Please replace the paragraph at page 18, lines 16 through 22 with the following paragraph:

Identity is often measured using sequence analysis software *e.g.*, BLASTN or BLASTP (available to the public on the world wide web at the web site of the National Center for Biotechnology Information (".ncbi"), National Library of Medicine (".nlm"), National Institutes of Health (".nih") of the United States government (".gov")). The default parameters for comparing two sequences (*e.g.*, "Blast"-ing two sequences against each other) by BLASTN (for nucleotide sequences) are reward for match = 1, penalty for mismatch = -2, open gap = 5, extension gap = 2. When using BLASTP for protein sequences, the default parameters are reward for match = 0, penalty for mismatch = 0, open gap = 11, and extension gap = 1.

Amendments to the specification are indicated in the attached "Marked Up Version of Amendments" (page i).

In the Claims

Please cancel Claims 36 and 38.

Please amend Claims 1, 6, 8-9, 14, 17, 22-23 and 25-26 as follows. Amendments to the claims are indicated in the attached "Marked Up Version of Amendments" (pages ii - iv).

1. (Amended) A method of producing a biologically active anti-angiogenic restin protein, or a biologically active mutant, fragment, derivative or fusion protein thereof, comprising:
 - (a) inserting an isolated polynucleotide comprising a polynucleotide sequence encoding an anti-angiogenic restin protein, or a mutant, derivative, fragment or fusion protein thereof, into a yeast expression vector, wherein the vector contains